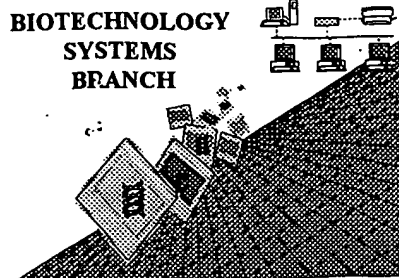


RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/378,045A
Source: 1646
Date Processed by STIC: 5/15/2001

RECEIVED

MAY 30 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

1646

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/378,045A

DATE: 05/15/2001

TIME: 09:43:32

Input Set : A:\2625-E Rev Seq List 04.24.01.txt

Output Set: N:\CRF3\05152001\I378045A.raw

2 <110> APPLICANT: Rauch, Charles
 3 Walczak, Henning
 5 <120> TITLE OF INVENTION: RECEPTOR THAT BINDS TRAIL
 6 <130> FILE REFERENCE: 2625-E
 8 <140> CURRENT APPLICATION NUMBER: US 09/378,045A
 9 <141> CURRENT FILING DATE: 1999-08-20
 11 <150> PRIOR APPLICATION NUMBER: US 08/883,036
 12 <151> PRIOR FILING DATE: 1997-06-26
 14 <150> PRIOR APPLICATION NUMBER: US 08/869,852
 15 <151> PRIOR FILING DATE: 1997-06-04
 17 <150> PRIOR APPLICATION NUMBER: US 08/829,536
 18 <151> PRIOR FILING DATE: 1997-03-28
 20 <150> PRIOR APPLICATION NUMBER: US 08/815,255
 21 <151> PRIOR FILING DATE: 1997-03-12
 23 <150> PRIOR APPLICATION NUMBER: US 08/799,861
 24 <151> PRIOR FILING DATE: 1997-02-13
 26 <160> NUMBER OF SEQ ID NOS: 5
 28 <170> SOFTWARE: PatentIn version 3.0/ Microsoft Word, Version 6.0.1

Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

310 <210> SEQ ID NO: 5
 311 <211> LENGTH: 8
 312 <212> TYPE: PRT
 C--> 313 <213> ORGANISM: Artificial
 315 <220> FEATURE:
 316 <223> OTHER INFORMATION: FLAG peptide
 318 <400> SEQUENCE: 5
 320 Asp Tyr Lys Asp Asp Asp Asp Lys
 321 1 5
 E--> 323

see item 11 on Ena Summary Sheet

delete at end of file

FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 05/15/2001

PATENT APPLICATION: US/09/378,045A

TIME: 09:43:33

Input Set : A:\2625-E Rev Seq List 04.24.01.txt

Output Set: N:\CRF3\05152001\I378045A.raw

L:6 M:283 W: Missing Blank Line separator, <130> field identifier
L:157 M:283 W: Missing Blank Line separator, <400> field identifier
L:279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:313 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:323 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/378,045A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

RECEIVED

MAY 30 2001

TECH CENTER 1600/2900

- 1 _____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 _____ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 _____ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 _____ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 _____ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 _____ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 _____ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 _____ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 _____ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 _____ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 _____ Use of "Artificial" (NEW RULES) Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.
- 12 _____ Use of <220>Feature (NEW RULES) Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 _____ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.